

Niche preferences and spatial distribution of Monogenea on the gills of *Pimelodus maculatus* in Río de la Plata (Argentina)

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SUMMARY

Five Monogenea species were found on the gills of the catfish *Pimelodus maculatus* in Río de la Plata (Argentina). These were used for studying the preference of species on different gill-hemibranches, niche breadth and niche overlap between species. It was found that congeneric species had a generic-specific preference for certain gill-hemibranches. Niche breadth appeared to be related to the number of individuals of each species. Niche overlap between the species is discussed.

Key words: *Demidospermus* ssp., *Scleroductus yuncensi*, *Pimelodus maculatus*, gill-hemibranch preferences, niche breadth, niche overlap.

INTRODUCTION

Most gill parasite communities tend to have lower species richness than gastrointestinal parasite communities of fish (Poulin, 1995). However, some gill monogenean communities have a high number of species (Koskivaara & Valtonen, 1992; Koskivaara, Valtonen & Vuori, 1992; Guegan & Hugueny, 1994; Rohde, 1994; Rohde *et al.* 1994). The monogenean community on the gills of the catfish *Pimelodus maculatus* is poor in terms of species richness (Gutiérrez & Martorelli, 1999). The advantage of studying communities of moderate species richness is that it is easier to interpret the observed phenomena and the intra- and interspecific relationships (Kennedy, 1990).

The niches and distribution microhabitat preferences of gill parasites have been studied in fish from the northern hemisphere (Suydam, 1971; Arme & Halton, 1972; Wootten, 1974; Hanek & Fernando, 1978; Adams, 1986; Buchmann, 1988*b*, 1989; Koskivaara *et al.* 1992). Rohde (1991) has proposed that for marine gill monogeneans intraspecific relationships are more important as niche-restricting factors than interspecific interactions. On the other hand, it has been established that the communities of fish parasites may be isolationist in nature, mainly because of the low species richness and intensity, which make vacant niches available (Kennedy, 1985; Dzika & Szymanski, 1989). It has also been observed

that the competition and interactive site segregation influence the structure of the communities (Buchmann, 1988*a*; Bates & Kennedy, 1990). The purpose of this study is to define the distribution of monogenean parasites on the gills of *P. maculatus*. In particular it needs to establish if the spatial resource is fully used and if there is niche overlap between the species.

MATERIALS AND METHODS

The fish were obtained by bottom net in Río de la Plata (Buenos Aires harbour), Argentina.

The *Pimelodus maculatus* (Lacépède, 1803) specimens were collected between May 1993 and April 1994. The fish were moved in PVC containers with permanent oxygenation and maintained alive until examined. The fish were sacrificed, weighed, and measured on the day they were collected. Gills were dissected immediately and placed in vials with an aceto-alcoholic solution (1:4). Individual parasites were removed from the gills with needles under a dissection microscope. All adult monogeneans were identified to species, after which the gill locations were registered. Gill location includes side; number and surface of the arch; number and third from each filament.

The gill-sectors are defined as sets of 10 adjacent gill filaments (Fig. 1). The absolute percentage of occupied sectors is the total number of gill-sectors occupied by a species in an individual host divided by the total number of gill-sectors of that host (including both infected and uninfected gill-sectors). The relative percentage of occupied sectors is the

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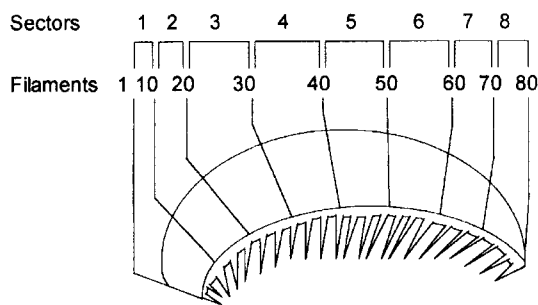


Fig. 1. Diagram showing gill sectors (set of 10 gill filaments) on the hemibranch of pimelodid fish.

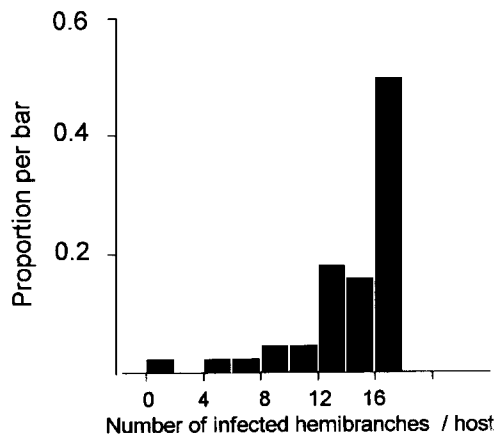


Fig. 2. Proportion of infected hemibranches per host (*Pimelodus maculatus*).

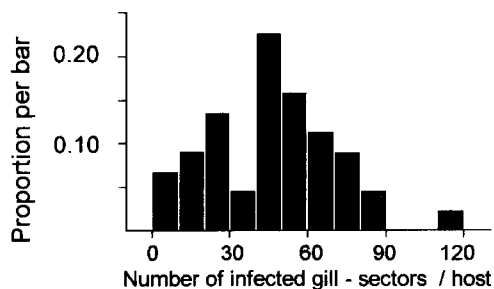


Fig. 3. Proportion of infected sectors per host (*Pimelodus maculatus*).

total number of gill-sectors occupied by a species in an individual host divided by the total number of occupied gill-sectors of that host examined (including infected gill-sectors only). These proportions are expressed as percentages. The specific niche breadth was measured using the measure of MacArthur-Levins (Lawlor, 1980) as proposed by Ludwig & Reynolds (1988). The specific niche breadth was computed as proposed by Koskivaara *et al.* (1992). To measure the overlap between species the equations of specific niche overlap proposed by Petraitis (1979, 1985) and Smith (1984) were used as suggested by Ludwig & Reynolds (1988).

Differences among measures were tested by the Kruskal–Wallis ANOVA, and differences between

measures were tested by the Mann–Whitney U-test. Statistical significance was judged at $P = 0.05$.

In this study the monogeneans of each host are considered to comprise an infracommunity and all infracommunities are considered as a component community (Bush & Holmes, 1986; Bush *et al.* 1997). Prevalence was used to determine core, secondary and satellite species (Hanski, 1982).

RESULTS

Five species of Monogenea were found in the 44 hosts examined: *Demiospermus uncusvalidus*, Gutiérrez & Suriano, 1992 (prevalence 90.9%), *D. armatus*, Kritsky & Gutiérrez, 1998 (79.5%), *D. paravalenciennesi*, Gutiérrez & Suriano, 1992 (97.7%), *D. bidiverticulatum*, (Suriano & Incorvaia, 1995) Kritsky & Gutiérrez, 1998 (79.5%) and *Scleroductus yuncensi*, Jara & Cone, 1989 (20.4%). *Demiospermus* species (Dactylogyridae: Ancyrocephalinae) were considered core species (prevalence over 70%) and *S. yuncensi* (Gyrodactylidae) at low prevalence can be considered a secondary species. There were no significant differences between the number of individuals of each species on the left and right gill arches (Mann–Whitney < 0.60 , $P > 0.54$).

A total of 704 hemibranches was examined, and 605 of those were infected (85.9%). The mean of the infected hemibranches per fish was 13.7 (s.d. 3.3). A total of 2019 (37.0%) gill-sectors was infected at the component community level. The mean of infected gill-sectors per fish was 45.9 (s.d. 22.9). A total of 50160 gill-filaments was examined and 3157 (6.3%) of those were infected. The mean of infected gill-filaments per host was 74.3 (s.d. 77.9). Each host has 1160 gill-filaments in average. At the component community level only 3.4% of the infected gill-filaments had more than a gill-filament third occupied by monogeneans. A total of 3265 (2.2%) gill-filament thirds was infected from the 150480 available gill-filament thirds.

The mean intensity at the component community was higher than 140.8 (s.d. 178.0) worms per fish. However, 14.1% of the hemibranches, 63.0% of the gill-sectors, 93.7% of the gill-filaments and 97.8% of the gill-filament thirds, were not infected.

Half of the hosts had all their hemibranches infected (Fig. 2). Except for 1 fish, all the hosts had more than 4 hemibranches infected (Fig. 2). None of the hosts had more than 111 sectors infected of the total of 124 on average available per fish (Fig. 3). Most infracommunities had less than 75% of the available gill-sectors infected (Fig. 3).

The median of hemibranches infected per host of each monogenean species was proportional to their mean intensity (Fig. 4). Except for *D. bidiverticulatum*, the core-species infected all the hemibranches

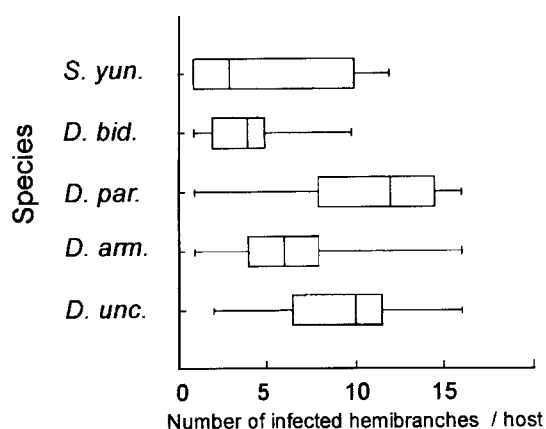


Fig. 4. Frequency distribution of infected hemibranches per host (*Pimelodus maculatus*). The vertical line inside the box represents the median, the vertical ends of the box represent the 25th and 75th percentiles and the vertical ends of the horizontal lines represent the lower and upper range. (*D. unc.* = *D. unicusvalidus*, *D. arm.* = *D. armostus*, *D. par.* = *D. paravalenciennesi*, *D. bid.* = *D. bidiverticulatum*, *S. yun.* = *S. yuncensi*).

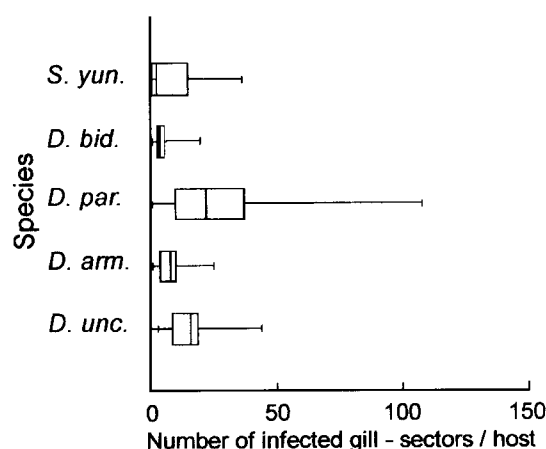


Fig. 5. Frequency specific distribution of infected sectors per host (*Pimelodus maculatus*). The vertical line inside the box represents the median, the vertical ends of the box represent the 25th and 75th percentiles and the vertical ends of the horizontal lines represent the lower and upper range. (*D. unc.* = *D. unicusvalidus*, *D. arm.* = *D. armostus*, *D. par.* = *D. paravalenciennesi*, *D. bid.* = *D. bidiverticulatum*, *S. yun.* = *S. yuncensi*).

of some host. *D. unicusvalidus* was the only species that infected at least 2 hemibranches in every host (Fig. 4). The secondary species, *S. yuncensi*, showed the lowest median of hemibranch infection per host. However, the range of hemibranch infection per host of this secondary species was wider than that of *D. bidiverticulatum*, a core-species.

Demidospermus paravalenciennesi had the widest range of infected gill-sectors (Fig. 5). However, no species occupied more than 50% of the available gill-sectors in every host. *D. unicusvalidus* infected at least 2 gill-sectors per host. *D. paravalenciennesi* showed 50% of mean absolute percentage of occupied sectors and 20% of mean relative percentage of occupied sectors (Table 1). The means of absolute and relative percentages of occupied sectors of *D. unicusvalidus* and *D. paravalenciennesi* were at least twice that of species of lower mean intensity (Table 1). *D. bidiverticulatum* showed less than 10% of mean relative percentage of occupied sectors and less than 5% of mean absolute percentage of occupied sectors (Table 1).

S. yuncensi did not show differences in infection on the hemibranches (KW = 1.22, $P = 0.99$). *Demidospermus* species showed significant differences in infection on the hemibranches (KW > 22.10, $P < 0.01$). The high and low preferences of hemibranches are presented in Fig. 6. The species with higher mean intensity (*D. unicusvalidus*, *D. armostus* and *D. paravalenciennesi*) shared a high preference for the hemibranches 1, 2, 3 and 4 (Fig. 6).

The niche breadth frequency distributions of each species are presented in Fig. 7. The median of the niche breadth by host of each species was proportional to their mean intensity. However, all the monogenean species show a wide range of niche breadth (Fig. 7). The measure of niche overlap requires that all species utilize all resources (i.e. no zeros in the data), because of the use of logarithms in their computation. This restriction limited the number of infracommunities included to calculate the niche overlap. *S. yuncensi* was not present in the selected infracommunities. The proportions of infracommunities in which the null hypothesis (complete overlap) was accepted are presented in Table 2. The

Table 1. Means of infected sectors, relative and absolute percentages of occupied sectors of monogeneans species and s.d. (in parentheses) per host (*Pimelodus maculatus*)

	Infected sectors	Relative percentage	Absolute percentage
<i>D. unicusvalidus</i>	15.6 (8.8)	30.2 (13.7)	12.6 (7.1)
<i>D. armostus</i>	8.0 (5.2)	16.6 (13.3)	6.5 (4.2)
<i>D. paravalenciennesi</i>	27.9 (20.6)	50.5 (18.3)	22.5 (16.6)
<i>D. bidiverticulatum</i>	5.2 (4.1)	9.2 (5.5)	4.2 (3.3)
<i>S. yuncensi</i>	9.5 (12.1)	12.4 (13.4)	7.7 (9.8)

	Hemibranches							
	1	2	3	4	5	6	7	8
<i>D. paravalen.</i>								
<i>D. uncusvalidus</i>								
<i>D. armostus</i>								
<i>D. bidivertic.</i>								

Fig. 6. High (shaded; KW < 6.52, $P > 0.09$) and low (KW < 5.57, $P > 0.06$) hemibranches infection in *Pimelodus maculatus*. (*D. uncusval.* = *D. uncusvalidus*, *D. bidivert.* = *D. bidiverticulatum*).

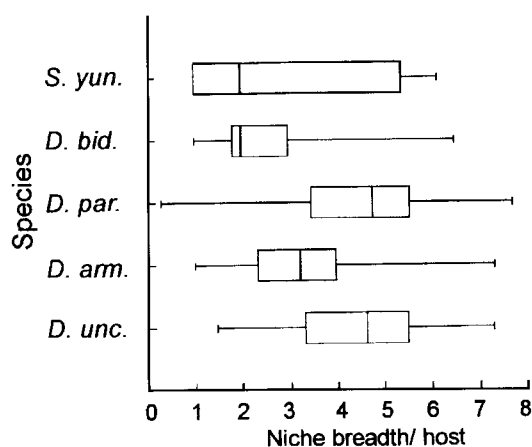


Fig. 7. Frequency specific distribution of niche breadth per host (*Pimelodus maculatus*). The vertical line inside the box represents the median, the vertical ends of the box represent the 25th and 75th percentiles and the vertical ends of the horizontal lines represent the lower and upper range. (*D. unc.* = *D. uncusvalidus*, *D. arm.* = *D. armostus*, *D. par.* = *D. paravalenciennesi*, *D. bid.* = *D. bidiverticulatum*, *S. yun.* = *S. yuncensi*).

Table 2. Percentage of infracommunities where the niche overlap by species in rows was complete onto species in column (statistic distributed as χ^2 below the critical value at $P = 0.05$)

(Number of computed co-occurrences ($n = 12$ infracommunities) indicated in parentheses. (*D. unc.* = *D. uncusvalidus*, *D. arm.* = *D. armostus*, *D. par.* = *D. paravalenciennesi*, *D. bid.* = *D. bidiverticulatum*)).

	<i>D. unc.</i>	<i>D. arm.</i>	<i>D. par.</i>	<i>D. bid.</i>
<i>D. unc.</i>	—	33.3 (9)	36.4 (11)	28.6 (7)
<i>D. arm.</i>	33.3 (9)	—	25.0 (8)	33.3 (6)
<i>D. par.</i>	27.3 (11)	25.0 (8)	—	28.6 (7)
<i>D. bid.</i>	28.6 (7)	66.7 (6)	28.6 (7)	—

proportion of niche overlap of a species with others was the same as the inverse situation, except for the pairs *D. uncusvalidus*–*D. paravalenciennesi* and *D. armostus*–*D. bidiverticulatum*. The mean niche overlap was 0.73 (s.d. = 0.20) and the 64.5 % of these values were higher than 0.5. However, 32.3 % of the niche overlap indices were significantly complete.

DISCUSSION

Rohde (1980) and Rohde, Hayward & Heap (1995) postulated that there exist many vacant niches in marine Monogenea communities. Most marine Monogenea belong to the subclass Monopisthocotylea (Oligonchoinea), whose size is greater than other Monopisthocotylea (Polyonchoinea). Due to these size differences the probability of finding high intensity of monogeneans in the marine environment is low. The Monogenea studied here are smaller in size. Therefore, the occupation pattern of the spatial resource is more intense. The detailed analysis carried out in this study confirms that there are many vacant niches in the Monogenea community on *P. maculatus*.

Gutiérrez & Martorelli (1994) indicated that *D. valenciennesi* showed a preference for the 2, 3, 4 and 5 hemibranches. This species is the only parasite species on the gills of the catfish *Parapimelodus valenciennesi* (Gutiérrez & Suriano, 1992). The spatial pattern preference of *D. valenciennesi* was related to both gill variables: gill area and water current over the gill hemibranches (Gutiérrez & Martorelli, 1994). The 2, 3, 4 and 5 hemibranches belong to the posterior hemibranch in the first gill arch, both hemibranches in the second gill-arch and the anterior hemibranch in third gill-arch. The water current is higher on the 2–3 and 4–5 pairs of hemibranches (Wootten, 1974). In this study all *Demidospermus* species showed a higher number of individuals on the 3 and 4 hemibranches. This situation indicates that most of the individuals of these species can be found on the second gill arch. The available area of this gill arch is the largest and it receives abundant dissolved oxygen in the water current.

Niche overlap indices are extensively used by ecologists. We use the niche overlap index proposed by Petraitis (1979, 1985) and Smith (1984) which is based on the comparison of the proportional usage of each resource by 2 species. The satellite-species was not included in the computation of the niche overlap index. The niche overlap index was utilized to measure the degree to which 2 species share the common gill resources. The few high overlap values for some species pairs indicate they were distributed according to habitat abundance. Species in the genus *Demidospermus* showed similar preferences for some hemibranches even though many sites on *P.*

maculatus remained empty. As Abrams (1990) and others noted, if resources are not scarce, there will not be negative interspecific interactions, regardless of the amount of niche overlap.

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